

FIGURE 1

Target segment starts with AA

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AAGATCCTCAAGAACATGACGCC [SEQ ID NO:18]	0.48	117	GAUCCUCAAGAAUGACGCCUU [SEQ ID NO:35] UUCUAGGAGUUCUUACUGCGG [SEQ ID NO:52]
AAGAATGACGCCCTACCGAAC [SEQ ID NO:19]	0.52	126	GAAUGACGCCUACCGAACUU [SEQ ID NO:36] UUCUUACUGCGGAUGGGGUUG [SEQ ID NO:53]
AACCGCATCATCAAGAACGAG [SEQ ID NO:20]	0.48	144	CCGCAUCAUCAAGAACGAGUU [SEQ ID NO:37] UUGGCGUAGUAGUUCUUGCUC [SEQ ID NO:54]
AAGAACGAGCTGAAGCTGCTG [SEQ ID NO:21]	0.52	156	GAACGAGCUGAAGCUGCUGUU [SEQ ID NO:38] UUCUUGCUCGACUUCGACGAC [SEQ ID NO:55]
AAGGAGCTGGCTATCATCCAC [SEQ ID NO:22]	0.52	381	GGAGCUGGCUAUCAUCCACUU [SEQ ID NO:39] UUCCUCGACCGAUAGUAGGUG [SEQ ID NO:56]
AAGCCTGAGAACATCATGCTG [SEQ ID NO:23]	0.48	411	GCCUGAGAACAUCAUGCUGUU [SEQ ID NO:40] UUCGGACUCUUGUAGUACGAC [SEQ ID NO:57]
AACATCATGCTGGTGACCAG [SEQ ID NO:24]	0.52	420	CAUCAUGCUGGUGGACCAGUU [SEQ ID NO:41] UUGUAGUACGACCACCUGGUC [SEQ ID NO:58]
AAGGTGATTGACTTCGGATCC [SEQ ID NO:25]	0.48	462	GGUGAUUGACUUCGGAUCCUU [SEQ ID NO:42] UUCCACUAACUGAAGCCUAGG [SEQ ID NO:59]
AAGGAGCCATACATCCAGTCG [SEQ ID NO:26]	0.52	513	GGAGCCAUCACAUCCAGUCGUU [SEQ ID NO:43] UUCCUCGGUAUGUAGGUAGCAGC [SEQ ID NO:60]

AACAAACGAGTACGACCAGGTG [SEQ ID NO:27]	0.52	651	CAACGAGUACGACCAGGUGUU [SEQ ID NO:44] UUGUUGCUCAUUGCUGGUCCAC [SEQ ID NO:61]
AAGTCGTTGGACCAGATTGAG [SEQ ID NO:28]	0.48	855	GUCGUUGGACCAGAUUGAGUU [SEQ ID NO:45] UUCAGCAACCUGGUCUAACUC [SEQ ID NO:62]
AAGAGCATGGTGGAGCTGATC [SEQ ID NO:29]	0.52	951	GAGCAUGGUGGAGCUGAUCUU [SEQ ID NO:46] UUCUCGUACCACCUUCGACUAG [SEQ ID NO:63]
AATGCGGTCTCCGACATGATG [SEQ ID NO:30]	0.52	1341	UGCGGUCUCCGACAUGAUGUU [SEQ ID NO:47] UUACGCCAGAGGCUGUACUAC [SEQ ID NO:64]
AAGTCCGACTCCAACTTCAGC [SEQ ID NO:31]	0.52	1485	GUCCGACUCCAACUUCAGCUU [SEQ ID NO:48] UUCAGGCUGAGGUUGAAGUCG [SEQ ID NO:65]
AACTTCAGCAACCTCATT CGG [SEQ ID NO:32]	0.48	1497	CUUCAGCAACCUCAUUCGGUU [SEQ ID NO:49] UUGAACUGGUUGGAGUAAGCC [SEQ ID NO:66]
AACATGACC ATGGAAGCTGAG [SEQ ID NO:33]	0.48	1647	CAUGACCAUGGAAGCUGAGUU [SEQ ID NO:50] UUGUACUGGUACCUUCGACUC [SEQ ID NO:67]
AATGGCTGAGTGAGCCAGACT [SEQ ID NO:34]	0.52	1711	UGGCUGAGUGAGCCAGACUUU [SEQ ID NO:51] UUACCGACUCACUCUGGUCUGA [SEQ ID NO:68]

Target segment starts with CA
Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
CAAGATCCTCAAGAATGACGC [SEQ ID NO:69]	0.48	116	AGAUCCUCAAGAAUGACGCCU [SEQ ID NO:89] UUUCUAGGAGUUCUUACUGCG [SEQ ID NO:109]
CAAGAATGACGCC TACCGCAA [SEQ ID NO:70]	0.52	125	AGAAUGACGCCUACCGCAAUU [SEQ ID NO:90] UUUCUUA CUGCGGAUGGCGUU [SEQ ID NO:110]

CAACCGCATCATCAAGAACGA [SEQ ID NO:71]	0.48	143	ACCGCAUCAUCAAGAACGAUU [SEQ ID NO:91] UUUGGCGUAGUAGUUCUUGC [SEQ ID NO:111]
CATCAAGAACGAGCTGAAGCT [SEQ ID NO:72]	0.48	152	UCAAGAACGAGCUGAAGCUUU [SEQ ID NO:92] UUAGGUUCUUGCUCGACUUCGA [SEQ ID NO:112]
CAAGAACGAGCTGAAGCTGCT [SEQ ID NO:73]	0.52	155	AGAACGAGCUGAAGCUGCUUU [SEQ ID NO:93] UUUCUUGCUCGACUUCGACGA [SEQ ID NO:113]
CATCCGCTTCCTTGAGTTCTT [SEQ ID NO:74]	0.48	215	UCCGCCUCCUUGAGUUCUUUU [SEQ ID NO:94] UUAGGCGAAGGAACUCAAGAA [SEQ ID NO:114]
CAGAAGGGAGAACAACTTCGCG [SEQ ID NO:75]	0.52	297	GAAGGGAGAACAAACUUCGCGUU [SEQ ID NO:95] UUCUUCCUCUUGUUGAAGCGC [SEQ ID NO:115]
CAAGGAGCTGGCTATCATCCA [SEQ ID NO:76]	0.52	380	AGGAGCUGGCUAUCAUCCAUU [SEQ ID NO:96] UUUCCUCGACCGAUAGUAGGU [SEQ ID NO:116]
CAAGCCTGAGAACATCATGCT [SEQ ID NO:77]	0.48	410	AGCCUGAGAACAUCAUGCUUU [SEQ ID NO:97] UUUCGGACUCUUGUAGUACGA [SEQ ID NO:117]
CAAGGTGATTGACTTCGGATC [SEQ ID NO:78]	0.48	461	AGGUGAUUGACUUCGGAUCUU [SEQ ID NO:98] UUUCCACUAACUGAAGCCUAG [SEQ ID NO:118]
CATACATCCAGTCGCGCTTCT [SEQ ID NO:79]	0.52	520	UACAUCCAGUCGCGCUUCUUU [SEQ ID NO:99] UUAUGUAGGUACAGCGCGAAGA [SEQ ID NO:119]
CAACAAACGAGTACGACCAGGT [SEQ ID NO:80]	0.52	650	ACAACGAGUACGACCAGGUUU [SEQ ID NO:100] UUUGUUGCUCAUGCUGGUCCA [SEQ ID NO:120]
CACCACTTCTTCAAGCGAAC [SEQ ID NO:81]	0.52	735	CCACUUUUCAAGCGAACUU [SEQ ID NO:101] UUGGUGAAGAAGUUCGCGUUG [SEQ ID NO:121]

CAAGTCGTTGGACCAGATTGA [SEQ ID NO:82]	0.48	854	AGUCGUUGGACCAGAUUGAUU [SEQ ID NO:102] UUUCAGCAACCUGGUACUACU [SEQ ID NO:122]
CAAGAGCATGGTGGAGCTGAT [SEQ ID NO:83]	0.52	950	AGAGCAUUGGUGGAGCUGAUUU [SEQ ID NO:103] UUUCUCGUACCACCUCGACUA [SEQ ID NO:123]
CAATCGGTCTCCGACATGAT [SEQ ID NO:84]	0.52	1340	AUGCGGUCUCCGACAUGAUUU [SEQ ID NO:104] UUUACGCCAGAGGCUGUACUA [SEQ ID NO:124]
CAAGTCGACTCCAACCTCAG [SEQ ID NO:85]	0.52	1484	AGUCCGACUCCAACUUUCAGUU [SEQ ID NO:105] UUUCAGGCUGAGGUUGAAGUC [SEQ ID NO:125]
CAACTTCAGCAACCTCATTG [SEQ ID NO:86]	0.48	1496	ACUUCAGCAACCUCAUUCGUU [SEQ ID NO:106] UUUGAAAGUCGUUGGAGUAAGC [SEQ ID NO:126]
CAACATGACCATGGAAGCTGA [SEQ ID NO:87]	0.48	1646	ACAUGACCAUGGAAGCUGAUU [SEQ ID NO:107] UUUGUACUGGUACCUUCGACU [SEQ ID NO:127]
CATGACCATGGAAGCTGAGAG [SEQ ID NO:88]	0.52	1649	UGACCAUGGAAGCUGAGAGUU [SEQ ID NO:108] UUACUGGUACCUUCGACUCUC [SEQ ID NO:128]

Target segment starts with GA

Target segment: 5' -> 3'

GC Ratio Position siRNA Sense strand: 5' -> 3'
siRNA Antisense strand: 3' -> 5'

GAGATGGTGGCCATCAAGATC [SEQ ID NO:129]	0.52	102	GAUGGUGGCCAUCAAGAUCUU [SEQ ID NO:144] UUCUACCAACCGGUAGUUCUAG [SEQ ID NO:159]
GATGGTGGCCATCAAGATCCT [SEQ ID NO:130]	0.52	104	UGGUGGCCAUCAAGAUCCUU [SEQ ID NO:145] UUAACCAACGGUAGUUCUAGGA [SEQ ID NO:160]
GATCCTCAAGAACATGACGCC [SEQ ID NO:131]	0.48	119	UCCUCAAGAACUGACGCC [SEQ ID NO:146] UUAGGAGUUCUUACUGCGGAU [SEQ ID NO:161]

GAGTCCAGAAGGAGAACAC [SEQ ID NO:132]	0.48	291	GUUCCAGAAGGAGAACACUU [SEQ ID NO:147] UUCAAGGUCUUCUCUUGUUG [SEQ ID NO:162]
GATCTAAGCCTGAGAACATC [SEQ ID NO:133]	0.48	405	UCUCAAGCCUGAGAACACUU [SEQ ID NO:148] UUAGAGUUCGGACUCUUGUAG [SEQ ID NO:163]
GAGAACATCATGCTGGTGGAC [SEQ ID NO:134]	0.52	417	GAACAUCAUUGCUGGUGGACUU [SEQ ID NO:149] UUCUUGUAGUACGACCACCGUG [SEQ ID NO:164]
GAACATCATGCTGGTGGACCA [SEQ ID NO:135]	0.52	419	ACAUCAUGCUGGUGGACCAUU [SEQ ID NO:150] UUUGUAGUACGACCACCUUGU [SEQ ID NO:165]
GAAGGAGCCATACATCCAGTC [SEQ ID NO:136]	0.52	512	AGGAGCCAUACAUCCAGUCUU [SEQ ID NO:151] UUUCCUCGGUAUGUAGGUCAG [SEQ ID NO:166]
GATTGAGACAGTGAATGGTGG [SEQ ID NO:137]	0.48	869	UUGAGACAGUGAAUGGUGGUU [SEQ ID NO:152] UUAACUCUGUCACUUACCACC [SEQ ID NO:167]
GAGACAGTGAATGGTGGCAGT [SEQ ID NO:138]	0.52	873	GACAGUGAAUGGUGGCAGUUU [SEQ ID NO:153] UUCUGUCACUUACCACCGUCA [SEQ ID NO:168]
GACAGTGAATGGTGGCAGTGT [SEQ ID NO:139]	0.52	875	CAGUGAAUGGUGGCAGUGUU [SEQ ID NO:154] UUGUCACUUACCACCGUCACA [SEQ ID NO:169]
GAGCATGGTGGAGCTGATCAA [SEQ ID NO:140]	0.52	953	GCAUGGUGGAGCUGAUCAUU [SEQ ID NO:155] UUCGUACCAACCGACUAGUU [SEQ ID NO:170]
GAGAAGGCACCAGGTATGCAA [SEQ ID NO:141]	0.52	1248	GAAGGCACCAGGUAGCAAUU [SEQ ID NO:156] UUCUUCGUGGUCCAUACGUU [SEQ ID NO:171]
GACTCCAACCTCAGCAACCTC [SEQ ID NO:142]	0.52	1491	CUCCAACUUCAGCAACCUCUU [SEQ ID NO:157] UUGAGGUUGAAGUCGUUGGAG [SEQ ID NO:172]

GACAACATGACCATGGAAGCT [SEQ ID NO:143]	0.48	1644	CAACAUGACCAUGGAAGCUUU [SEQ ID NO:158] UUGUUGUACUGGUACCUUCGA [SEQ ID NO:173]
Target segment starts with TA			
Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
TACCGCAACCGCATCATCAAG [SEQ ID NO:174]	0.52	138	CCGCAACCGCAUCAUCAAGUU [SEQ ID NO:180] UUGGCGUUGGCGUAGUAGUUC [SEQ ID NO:186]
TACGTGAAGGAGGCCATACATC [SEQ ID NO:175]	0.48	507	CGUGAAGGAGCCAUCAUCAUCUU [SEQ ID NO:181] UUGCACUUCCUCGGUAUGUAG [SEQ ID NO:187]
TACATCCAGTCGCGCTTCTAC [SEQ ID NO:176]	0.52	522	CAUCCAGUCGCGCUUCUACUU [SEQ ID NO:182] UUGUAGGUACAGCGCGAAGAUG [SEQ ID NO:188]
TATGCTCAAGTCGTTGGACCA [SEQ ID NO:177]	0.48	848	UGCUCAGUCGUUGGACCAUU [SEQ ID NO:183] UUACGAGUUUCAGCAACCUGGU [SEQ ID NO:189]
TACTACTGTCTGGCTGAGGAG [SEQ ID NO:178]	0.52	1173	CUACUGUCUGGCUGAGGAGUU [SEQ ID NO:184] UUGAUGACAGACCGACUCCUC [SEQ ID NO:190]
TACTGTCTGGCTGAGGAGAAAG [SEQ ID NO:179]	0.52	1176	CUGUCUGGCUGAGGAGAAAGUU [SEQ ID NO:185] UUGACAGACCGACUCCUCUUC [SEQ ID NO:191]

FIGURE 2

A

Protein Sequence of Human HIPK4

Total length -- 616 AA

MSTIQSETDCYDIIIEVLGKGTGEVAKGWRRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE
LQNLFEFQKENNFAPLPARHIRTVTQLQVLTALARLKELAIIHADLKOPENIMLVQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRYRAPEIILGLPCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLL
AACKAHFFKRNPDAANPWQLKSSADYLAETKVRPLERRKMLKSLDQIETVNGGSVASRLTFPDREALAEHDLKSM
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHETTHYYQLSLRSYRLSILQVEGKPPTPVAAEDGTPYYCLAEKE
AAGMGSVAGSSPFFFREEKAPGMQRRAIDQLDDLSLQEAGHGLWGETCTNAVSDMMVPLKAAITGHHPDSGPEPILAFYSS
RLAGRHKARKPPAGSKSDNSNLIQLSQVSPEDDRPCRGSSWEEGEHLGASAEPPLAILQRDEDGPNIIDNMTMEAERPDP
ELFDPSSCPGEWLSEPDCTLESVRGPRAQGLPPRRSHQHGPPRGATTSFLQHVTGHH

B

ATP Binding Domain -- 17-40 (predicted)

LKGKTFGEVAKGWRRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKOPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGEVAKGWRRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE
LQNLFEFQKENNFAPLPARHIRTVTQLQVLTALARLKELAIIHADLKOPENIMLVQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRYRAPEIILGLPCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHFFK
RNPHPDAANPWQLKSSADYLAETKVRPLERRKMLKSLDQIETVNGGSVASRLTFPDREALAEHDLKSMVELIKRMLTW
ESHERISPSAALRHPFV

FIGURE 3

A

Protein Sequence of Mouse HIPK4

Total length -- 616 AA

MATIQSETDCYDIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRSRIIKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKPEINMLVDQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPCEKVDVSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH
AARKAHFFKRNPHPDATNPWQLKSSADYLAETKVRPLERRKYMMLKSLDQIETVNGGAVSRLSFDPREALAEHADLKS
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHEATRYYQSLRGCRSLIQVGDKPPPPVIASAEDGPPYYRLAEEE
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMVSDLMLVPLKVASTSHRPDSGPEPILAFYG
SRLTGRHKARKAPAGSKSDNSNFSNLIRLSQASPEDAGPCRGSGWEEGEGRTTSTEPSVIPQREGDGPGIKDRPMDAERPG
PELFDPSSCPGEWLSEPEWTLEGIRGSRAQGLPAHHPHGPPRTTSFLQHVGGHH

B

ATP Binding Domain -- 17-40 (predicted)

LKGKGTGGEVAKGWRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKPEINML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRSRIIKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LLEQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKPEINMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRFYRAPEILLGLPCEKVDVSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAAARKAHFFK
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYMMLKSLDQIETVNGGAVSRLSFDPREALAEHADLKS
MVELIKRMLTWESHERISPSAALRHPFV

358212v1 [MSWord]

FIGURE 4

A

Protein Sequence of Monkey HIPK4

Total length -- 616 AA

MATTQSETDCYDIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFELLEQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKOPENIMLVQDQTRCPFRVKVIDFGSASIFSEVRYVKEPYIQSRSFYRAPEILLGLPCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFKRNPDAANPWQLKSSADYLAETKVRPLERRKYMlKSLDQIETVNGGSVASRLTFPDREALAEHDLKSMVELIKRMLTWESHERISPSAALRHPFVSMQQLRNAHETTHYYQLSLRSYRLSLQVEGKPPAPVVAEEDGTPYYRLAEEKEAAGMGSVASSSPFFREEKAPGMQRAIDQLDDLSLQEAGHGLWGETCTDVSDMMAPLKAATGRHMPDSGPEPILAFYSSRLAGRHKARKPPAGSKSDSNLSNLIRLSQVSPEDDRPCRGSSWEEGEHLGASAEPAILQRDGDPNIDNMTMEAERPDPELFDPSSCPGEWLSEPDWTLEGVRGPRAQGLPPRRSHQHGPPRGATSFHQVTGHH

B

ATP Binding Domain -- 17-40 (predicted)

LGKGTGGEVAKGWRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKOPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE LLEQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKOPENIMLVQDQTRCPFRVKVIDFGSASIFSEVRY VKEPYIQSRSFYRAPEILLGLPCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFKRNPDAANPWQLKSSADYLAETKVRPLERRKYMlKSLDQIETVNGGSVASRLTFPDREALAEHDLKSMVELIKRMLTWESENISPSAALRHPFV

FIGURE 5

A

Protein Sequence of Rat HIPK4

Total length -- 616 AA

MATIQSETDCYDIIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRSRIIKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LLEQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKPE
NIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRYRAPEILLGLPFCEKV
DWVSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHHFFK
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYM
LKS
LDQIETVNGGGAVSRLSF
PDREALAEHADLKSMVELIKRMLTWE
SHERISPSAALRHPFV
SMQQLRSAHEATRYYQLSLRGCR
LSI
QVDGK
PPP
VIA
SAEDGPP
YRLAEEE
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMV
SDMLVPLK
VASTSHRV
PDSGPE
PILAFYG
SRLTGRHKARKAPAGSKSDNSFNLIRLSQASPEDAGPCRGSG
WEE
GEGR
TT
STE
PSVI
PQREGDGPGIKDRPM
DAERPG
PELFDPSSCPGEWLSEPEWTLEGIRGSRAQGLPAHHPHGPPRTTSFLQHVGGHH

B

ATP Binding Domain -- 17-40 (predicted)

LKGKGTGGEVAKGWRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I
I
HADLKPE
NIMLV

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGGEVAKGWRSTGEMVAIKILKNDAYRSRIIKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LLEQNLFEFQKENNFAPLPARHIRTVTLQVLRALARLKELAIIHADLKPE
NIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRYRAPEILLGLPFCEKV
DWVSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHHFFK
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYM
LKS
LDQIETVNGGGAVSRLSF
PDREALAEHADLKSMVELIKRMLTWE
SHERISPSAALRHPFV
SMQQLRSAHEATRYYQLSLRGCR
LSI
QVDGK
PPP
VIA
SAEDGPP
YRLAEEE
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMV
SDMLVPLK
VASTSHRV
PDSGPE
PILAFYG
SRLTGRHKARKAPAGSKSDNSFNLIRLSQASPEDAGPCRGSG
WEE
GEGR
TT
STE
PSVI
PQREGDGPGIKDRPM
DAERPG
PELFDPSSCPGEWLSEPEWTLEGIRGSRAQGLPAHHPHGPPRTTSFLQHVGGHH

FIGURE 6

A

CLUSTAL W multiple sequence alignment results

MSF: 346 Type: P Check: 4900 ..

Name: mushipk3_np_034564.kd.pep oo Len: 346 Check: 9189 Weight: 7.5
Name: rathipk3_np_113975.kd.fas.pep oo Len: 346 Check: 347 Weight: 6.5
Name: humhipk3_np_005725.kd.pep oo Len: 346 Check: 9094 Weight: 7.8
Name: humhipk1-like_ax318266.kd.pep oo Len: 346 Check: 773 Weight: 6.8
Name: mushipk1_np_034562.kd.pep oo Len: 346 Check: 878 Weight: 7.0
Name: humhipk2_np_073577.kd.fas.pep oo Len: 346 Check: 11 Weight: 6.7
Name: mushipk2_np_034563.kd.pep oo Len: 346 Check: 1047 Weight: 7.7
Name: wormf20b6_q19632.kd.pep oo Len: 346 Check: 9639 Weight: 16.4
Name: humhipk4.kd.fas.pep oo Len: 346 Check: 4355 Weight: 5.4
Name: monkeyhipk4_ab074449.kd.fas.pep oo Len: 346 Check: 4346 Weight: 5.3
Name: mushipk4.kd.fas.pep oo Len: 346 Check: 5897 Weight: 5.4
Name: rathipk4_xp_218355.kd.fas.pep oo Len: 346 Check: 5822 Weight: 4.8
Name: yeastyak1_np_012394.kd.fas.pep oo Len: 346 Check: 3415 Weight: 12.2
Name: dmcg17090_q95tg3.kd.pep oo Len: 346 Check: 87 Weight: 26.0

//

1 50
mushipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIK ILKNHPSYAR QQQIEVSILA
rathipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIK ILKNHPSYAR QQQIEVSILA
humhipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIK ILKNHPSYAR QQQIEVSILA
humhipk1-lik YEVLEFLGRG TFGQVAKCWK RSTKEIVAIK ILKNHPSYAR QQQIEVSILS
mushipk1_np_ YEVLEFLGRG TFGQVAKCWK RSTKEIVAIK ILKNHPSYAR QQQIEVSILS
humhipk2_np_ YEVLEFLGRG TFGQVVKCWK RGTNEIVAIK ILKNHPSYAR QQQIEVSILA
mushipk2_np_ YEVLEFLGRG TFGQVVKCWK RGTNEIVAIK ILKNHPSYAR QQQIEVSILA
wormf20b6_q1 YEVLEFLGKG TFGQVVKAWK KGTSEIVAIK ILKKHPSYAR QQQIEVSILS
humhipk4.kd. YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
monkeyhipk4_ YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
mushipk4.kd. YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
rathipk4_xp_ YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
yeastyak1_np_ YLVLDILGQG TFGQVVKCQN LLTKEILAVK VVKSRTTEYLT QSITEAKILE
dmcg17090_q9 ...YIFNCLD DIGQNVPTD LEGGQLLAEK TDRREFIDLL KRMLTIDQER

51 100
mushipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLVD FLKQNKFSP
rathipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLVD FLKQNKFSP
humhipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLVD FLKQNKFSP
humhipk1-lik RLSSENA..D EYNFVRSYEC FQHKNHTCLV FEMLEQNLVD FLKQNKFSP
mushipk1_np_ RLSSENA..D EYNFVRSYEC FQHKNHTCLV FEMLEQNLVD FLKQNKFSP
humhipk2_np_ RLSTESA..D DYNFVRAYEC FQHKNHTCLV FEMLEQNLVD FLKQNKFSP
mushipk2_np_ RLSTESA..D DYNFVRAYEC FQHKNHTCLV FEMLEQNLVD FLKQNKFSP
wormf20b6_q1 RLSNENS..E EFNFVRAFEC FNHKSHTCLV FEMLEQNLVD FLKQNKFMP
humhipk4.kd. CMRGGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLFE FQKENNFAPL
monkeyhipk4_ CMRGGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLFE FQKENNFAPL
mushipk4.kd. CVRGLDP..D EAHVIRFLEF FHDALKFYLV FELLEQNLFE FQKENNFAPL
rathipk4_xp_ CVRGLDP..D EAHVIRFLEF FHDALKFYLV FELLEQNLFE FQKENNFAPL
yeastyak1_np_ LLNQKIDPTN KHHFLRMYDS FVHKNHLCVL FELLSNNLYE LLKQNKFHGL
dmcg17090_q9 RLTPAEALNH SFTRLTHLVD YVYCNNVKAS VQMMEVCRG DFHTVQPAST

	101		150			
mushipk3_np_	PLKVIRPVLO	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID	
rathipk3_np_	PLKVIRPVLO	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID	
humhipk3_np_	PLKVIRPILQ	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID	
humhipk1-lik	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID	
mushipk1_np_	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID	
humhipk2_np_	PLKYIRPVLQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPDPS	RQPYRVKVID	
mushipk2_np_	PLKYIRPVLQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPDPS	RQPYRVKVID	
wormf20b6_q1	PLNAIRPILF	QVLTALLKLK	SLGLIHADLK	PENIMLVDPQ	QQPYRVKVID	
humhipk4.kd.	PARHIRTVTL	QVLALARLK	ELAIIHADLK	PENIMLVVDQT	RCPFRVKVID	
monkeyhipk4_	PARHIRTVTL	QVLRALARLK	ELAIIHADLK	PENIMLVVDQT	RCPFRVKVID	
mushipk4.kd.	PARHIRTVTL	QVLRALARLK	ELAIIHADLK	PENIMLVVDQT	RCPFRVKVID	
rathipk4_xp_	PARHIRTVTL	QVLRALARLK	ELAIIHADLK	PENIMLVVDQT	RCPFRVKVID	
yeastyak1_np	SIQLIRTFTT	QILDSCLCVLK	ESKLIHCDLK	PENILLCAPD	KP..ELKIID	
dmcg17090_q9	LVTNFVPSSST	ENMTFTINNQ	LTSQVQLRVR	DGRPLAYEGL	YQIYNGRSVA	
	151		200			
mushipk3_np_	FGSASHVSKT	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
rathipk3_np_	FGSASHVSKT	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
humhipk3_np_	FGSASHVSKT	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
humhipk1-lik	FGSASHVSKA	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
mushipk1_np_	FGSASHVSKA	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
humhipk2_np_	FGSASHVSKA	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
mushipk2_np_	FGSASHVSKA	..VCSTYLSQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL	
wormf20b6_q1	FGSASHRSKA	..VTNTYLSQS	RYYRAPEIIL	GLPFNESIDM	WSLGCVIAEL	
humhipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPCEKVDV	WSLGCVMAEL	
monkeyhipk4_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPCEKVDV	WSLGCVMAEL	
mushipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPCEKVDV	WSLGCVMAEL	
rathipk4_xp_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPCEKVDV	WSLGCVMAEL	
yeastyak1_np	FGSSCEEART	...VYTYIQS	RFYRAPEIIL	GIPYSTSIDM	WSLGCVIAEL	
dmcg17090_q9	RQYP.....QRTTDS	FQHQLVSNIL	CPPSYQTMPS	PTKHVVVGSA	
	201		250			
mushipk3_np_	FLGWPLYPGA	LEHDQIRYIS	QTQGLPGEQL	LNVGKSTRF	FCRE.....	
rathipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL	LNVGKSTRF	FCRE.....	
humhipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL	LNVGKSTRF	FCKE.....	
humhipk1-lik	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....	
mushipk1_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....	
humhipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....	
mushipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....	
wormf20b6_q1	FLGWPLYPGS	SEYDQIRFII	QTQGLPPTSM	LESASKLHRF	FKEVKSESPN	
humhipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAACKAHHF	FKRNP.....	
monkeyhipk4_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAARKAHHF	FKRNP.....	
mushipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAARKAHHF	FKRNP.....	
rathipk4_xp_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAARKAHHF	FKRNP.....	
yeastyak1_np	FLGIPIFPGA	SEYNQLTRII	DTLGYPNSWM	IDMGKNSGKF	MKKLAPEE..	
dmcg17090_q9	TMQPPLQVPP	QQYVNVPVPV	SMVEPTSGQR	MLLTNRVQAS	GVAWPQTG..	

251

300

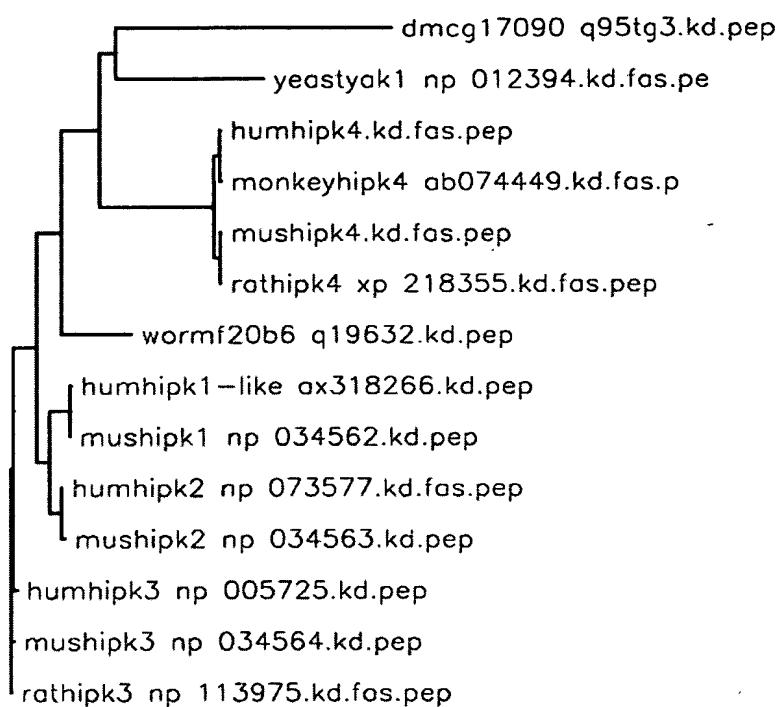
mushipk3_np_ . TDMSHSGWR LKTLEEHEAE TG.MKSKEAR KYIFNSLDDI VHVN.....T
 rathipk3_np_ . TDMSHSGWR LKTLEEHEAE TG.MKSKEAR KYIFNSLDDI VHVN.....T
 humhipk3_np_ . TDMSHSGWR LKTLEEHEAE TG.MKSKEAR KYIFNSLDDV AHVN.....T
 humhipk1-lik . PNLYGPLWR LKTPEEHELE TG.IKSKEAR KYIFNCLDDM AQVN.....M
 mushipk1_np_ . PNLYGPLWR LKTPEEHELE TG.IKSKEAR KYIFNCLDDM AQVN.....M
 humhipk2_np_ . TDSPYPLWR LKTPDDHEAE TG.IKSKEAR KYIFNCLDDM AQVN.....M
 mushipk2_np_ . TDSPYPLWR LKTPDDHEAE TG.TKSKEAR KYIFNCLDDM AQGN.....M
 wormf20b6_q1 HTNVGGSYYR LKTVEEYEAS SSTAJSKETR KYIFNVIDDI SRVC.....Y
 humhipk4.kd. . HPDAANPWFQ LKSSADYLAE TK.VRPLERR KYMLKSLDQI ETVNGGSVAS
 monkeyhipk4_ . HPDAANPWFQ LKSSADYLAE TK.VRPLERR KYMLKSLDQI ETVNGGSVAS
 mushipk4.kd. . HPDATNPWFQ LKSSADYLAE TK.VRPLERR KYMLKSLDQI ETVNGGGAVS
 rathipk4_xp_ . HPDATNPWFQ LKSSADYLAE TK.VRPLERR KYMLKSLDQI ETVNGGGAVN
 yeastyak1_np . SSSSTQKHR MKTIEFCRE YNIVEKPSKQ YFKWRKLPDI IRNYR..YPK
 dmchg17090_q9 RQMALVPSWP QQAPAHSLIV DSTPLFNVEE IYPKHHLNLP RNDLKKESPA

301

346

mushipk3_np_ VMDLEGGDLL AEKADRREFV NLLKKMLLID ADLRITPIET LNHPFV
 rathipk3_np_ VMDLEGSDLL AEKADRREFV SLLKKMLLID ADLRITPIET LNHPFV
 humhipk3_np_ VMDLEGSDLL AEKADRREFV SLLKKMLLID ADLRITPAET LNHPFV
 humhipk1-lik STDLEGTDML AEKADRREYI DLLKKMLTID ADKRITPLKT LNHQFV
 mushipk1_np_ STDLEGTDML AEKADRREYI DLLKKMLTID ADKRITPLKT LNHQFV
 humhipk2_np_ TTDLEGSDML VEKADRREFI DLLKKMLTID ADKRITPIET LNHPFV
 mushipk2_np_ TTDLEGSDML VEKADRREFI DLLKKMLTID ADKRVTPIET LNHPFV
 wormf20b6_q1 GFESDPVEHL CDRIDRQEFL DVLKKMLVNL PDFRITPAEG LESKFV
 humhipk4.kd. RLTFPDREAL AEHADLKSMV ELIKRMLTWE SHERISPSAA LRHPFV
 monkeyhipk4_ RLTFPDREAL AEHADLKSMV ELIKRMLTWE SHERISPSAA LRHPFV
 mushipk4.kd. RLSFPDREAL AEHADLKSMV ELIKRMLTWE SHERISPSAA LRHPFV
 rathipk4_xp_ RLSFPDREAL AEHADLKSMV ELIKRMLTWE SHERISPSAA LRHPFV
 yeastyak1_np SIQNSQELID QEMQNRECLI HFLGGVLNLN PLERWTPQQA MLHPFI
 dmchg17090_q9 HHIAKGNSYR VPRHEKKEHQ QLSPVKKRVK ESSPPHQQRY QRAAHV

B



412288v1 [MS Word]

FIGURE 7

A

CLUSTAL W multiple sequence alignment results

MSF: 340 Type: P Check: 1950 ..

Name: musdyrk1a_np_031916.kd.pep oo Len: 340 Check: 8276 Weight: 2.2
Name: ratdyrk1a_np_036923.kd.pep oo Len: 340 Check: 8276 Weight: 2.2
Name: humdyrk1a_np_001387.kd.pep oo Len: 340 Check: 8161 Weight: 2.2
Name: humdyrk1b_np_004705.kd.pep oo Len: 340 Check: 7992 Weight: 3.5
Name: musdyrk1b_np_034222.kd.pep oo Len: 340 Check: 6091 Weight: 2.6
Name: dmmnb_aaf48776.kd.pep oo Len: 340 Check: 7580 Weight: 5.3
Name: wormt04c10_q22155.kd.pep oo Len: 340 Check: 9628 Weight: 8.0
Name: dmssmi35a_q9v3d5.kd.pep oo Len: 340 Check: 6217 Weight: 8.4
Name: humdyrk4_dyr4_human.kd.pep oo Len: 340 Check: 1420 Weight: 8.0
Name: humdyrk2_np_006473.kd.pep oo Len: 340 Check: 8233 Weight: 6.6
Name: humdyrk3_np_003573.kd.pep oo Len: 340 Check: 8166 Weight: 7.5
Name: wormf49e11_q20604.kd.pep oo Len: 340 Check: 7542 Weight: 7.5
Name: kab7_schpo.kd.pep oo Len: 340 Check: 9798 Weight: 11.1
Name: pom1_schpo.kd.pep oo Len: 340 Check: 8379 Weight: 9.8
Name: humhipk4.kd.pep oo Len: 340 Check: 8285 Weight: 3.5
Name: monkeyhipk4_ab074449.kd.fas.pe oo Len: 340 Check: 8293 Weight: 3.5
Name: mushipk4.kd.pep oo Len: 340 Check: 9829 Weight: 3.5
Name: rathipk4_xp_218355.kd.pep oo Len: 340 Check: 9784 Weight: 3.5

//

1

50

musdyrk1a_np YEIDSLIGKG SFGQVVVKAYD RVEQEWAIK IIKNKKAFLN QAQIEVRLLE
ratdyrk1a_np YEIDSLIGKG SFGQVVVKAYD RVEQEWAIK IIKNKKAFLN QAQIEVRLLE
humdyrk1a_np YEIDSLIGKG SFGQVVVKAYD RVEQEWAIK IIKNKKAFLN QAQIEVRLLE
humdyrk1b_np YEIDSLIGKG SFGQVVVKAYD HQTQELVVAIK IIKNKKAFLN QAQIELRLLE
musdyrk1b_np YEIDSLIGKG SFGQVVVKAYD HQTQELVVAIK IIKNKKAFLN QAQIELRLLE
dmmnb_aaf487 YEIDSLIGKG SFGQVVVKAYD HEEQCHVVAIK IIKNKKPFLN QAQIEVKLL
wormt04c10_q ILSDTPVGKG SFGQVTKAYD TLNKEEVAIK IIKNKKTFFD QAQIEIHLLE
dmssmi35a_q9v YEILEVIGKG SFGQVIRALD HKTNTHVAIK IIRNKKRFLN QAVVELNILD
humdyrk4_dyr YEVLETIGKG SFGQVAKCLD HKNNELVALK IIRNKKRFHQ QALMELKILE
humdyrk2_np_ YEVLKVIDGKG SFGQVVVKAYD HKVHQHVALK MVRNEKRFHR QAAEEIRILE
humdyrk3_np_ YEVLCIIGKG SFGQVARVYD HKLRQYVALK MVRNEKRFHR QAAEEIRILE
wormf49e11_q YEVLKVIDGKG SFGQVIKAFD HKYQQYVALK LVRNEKRFHR QADEEIRILD
kab7_schpo.k YEIIDTVGKG SFGQVLKCID HKRGQVVAIK VIKNRQKFHG QTLVEVGILK
pom1_schpo.k YEVVDFLGKG SFGQVLRCID YETGKLVALK IIRNKKRFHM QALVETKILQ
humhipk4.kd. YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
monkeyhipk4_ YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
mushipk4.kd. YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
rathipk4_xp_ YDIIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR

51

100

musdyrk1a_np LMNKHDTEMK YYIVHLKRHF MFRNHLCLVF EMLSYNLYDL LRNTNFRGVS
 ratdyrk1a_np LMNKHDTEMK YYIVHLKRHF MFRNHLCLVF EMLSYNLYDL LRNTNFRGVS
 humdyrk1a_np LMNKHDTEMK YYIVHLKRHF MFRNHLCLVF EMLSYNLYDL LRNTNFRGVS
 humdyrk1b_np LMNQHDTEMK YYIVHLKRHF MFRNHLCLVF ELLSYNLYDL LRNTHFRGVS
 musdyrk1b_np LMNQHDTEMK YYIVHLKRHF MFRNHLCLVF ELLSYNLYDL LRNTHFRGVS
 dmmnb_aaf487 MMNRADAENK YYIVKLKRHF MWRNHLCLVF ELLSYNLYDL LRNTNFRGVS
 wormt04c10_q LTNAHKDKNK YNIVTLKGHF VHRAHLCLVF ELLSYNLYDL LKNTSFRGVS
 dmsmi35a_q9v ELREKDADGS HNVIHMLDYT YFRKHLCITF ELMSLNLYEL IKKNNYNGFS
 humdyrk4_dyr ALRKKDKDNT YNVVHMKDFF YFRNHFCITF ELLGINLYEL MKNNNFQGFS
 humdyrk2_np_ HLRKQDKDNT MNVIHMLENF TFRNHICMTF ELLSMNLYEL IKKNKFQGFS
 humdyrk3_np_ HLKKQDKTGS MNVIHMLESF TFRNHVCMAF ELLSIDLYEL IKKNKFQGFS
 wormf49e11_q HLRRQDSDT HNIIHMLDYF NFRNHKCITF ELLSINLYEL IKRNKFQGFS
 kab7_schpo.k RLCEADPADK NNVIRYLSHF DFRGHLCIVT ELLGSNLFDV IRENNYKGLP
 pom1_schpo.k KIREWDPD E YCMVQYTDHF YFRDHLCVAT ELLGKNLYEL IKSNGFKGLP
 humhipk4.kd. CMRGLDPE.E AHVIRFLEFF HDALKFYLVF ELLEQNLFEF QKENNFAPLP
 monkeyhipk4_ CMRGLDPE.E AHVIRFLEFF HDALKFYLVF ELLEQNLFEF QKENNFAPLP
 mushipk4.kd. CVRGLDPD.E AHVIRFLEFF HDALKFYLVF ELLEQNLFEF QKENNFAPLP
 rathipk4_xp_ CVRGLDPD.E AHVIRFLEFF HDALKFYLVF ELLEQNLFEF QKENNFAPLP

101

150

musdyrk1a_np LNLTRKFAQQ MCTALLFLAT PELSIIHCDL KPENILLCNP KRS..AIKIV
 ratdyrk1a_np LNLTRKFAQQ MCTALLFLAT PELSIIHCDL KPENILLCNP KRS..AIKIV
 humdyrk1a_np LNLTRKFAQQ MCTALLFLAT PELSIIHCDL KPENILLCNP KRS..AIKIV
 humdyrk1b_np LNLTRKLAQQ LCTALLFLAT PELSIIHCDL KPENILLCNP KRS..AIKIV
 musdyrk1b_np LNLTRKLAQQ LCTALLFLAT PELSIIHCDL KPENILLCNP KRS..AIKIV
 dmmnb_aaf487 LNLTRKFAQQ LCTALLFLST PELNIIHCDL KPENILLCNP KRS..AIKIV
 wormt04c10_q LNLARKFAQQ LGKTLLFLSS PELSIIHCDL KPENVLLVNA KRS..QIRVI
 dmsmi35a_q9v MSLIRRFCNS IVKCLRLLY. .KENIIHCDL KPENILLKQR GSS..SIKVI
 humdyrk4_dyr LSIVRRFTLS VLKCLQMLS. .VEKIIHCDL KPENIVLYQK GQA..SVKVI
 humdyrk2_np_ LPLVRKFAHS ILQCLDALH. .KNRIIHCDL KPENILLKQQ GRS..GIKVI
 humdyrk3_np_ VQLVRKFAQS ILQSLDALH. .KNKIIHCDL KPENILLKHH GRS..STKVI
 wormf49e11_q LMLVRKFAYS MLLCLDLLQ. .KNRLIHCDL KPENVLLKQQ GRS..GIKVI
 kab7_schpo.k LIVVKSFALQ GLQALRLLQ. .GQNIIHCDL KPENLLLSPH LKA..RIKLI
 pom1_schpo.k IVVIKSITRQ LIQCLTLLN. .EKHVIHCDL KPENILLCHP FKS..QVKVI
 humhipk4.kd. ARHIRTVTLQ VLTALARLK. .ELAIIHADL KPENIMLVDQ TRCPFRVKVI
 monkeyhipk4_ ARHIRTVTLQ VLRALARLK. .ELAIIHADL KPENIMLVDQ TRCPFRVKVI
 mushipk4.kd. ARHIRTVTLQ VLRALARLK. .ELAIIHADL KPENIMLVDQ TRCPFRVKVI
 rathipk4_xp_ ARHIRTVTLQ VLRALARLK. .ELAIIHADL KPENIMLVDQ TRCPFRVKVI

151	200
musdyrk1a_np DFGSSCQLGQ R...IYQYIQ SRFYRSPEVL LGMPYDLAID MWSLGCILVE	
ratdyrk1a_np DFGSSCQLGQ R...IYQYIQ SRFYRSPEVL LGMPYDLAID MWSLGCILVE	
humdyrk1a_np DFGSSCQLGQ R...IYQYIQ SRFYRSPEVL LGMPYDLAID MWSLGCILVE	
humdyrk1b_np DFGSSCQLGQ R...IYQYIQ SRFYRSPEVL LGTPYDLAID MWSLGCILVE	
musdyrk1b_np DFGSSCQLGQ R...IYQYIQ SRFYRSPEVL LGTPYDLAID MWSLGCILVE	
dmmnb_aaf487 DFGSSCQLGQ R...IYHYIQ SRFYRSPEVL LGIQYDLAID MWSLGCILVE	
wormt04c10_q DFGSSCQTGH R...IYQYIQ SRFYRSPEVL LGIAYDTKID MWSLGCILVE	
dmsmi35a_q9v DFGSSCYVDR K...IYTYIQ SRFYRSPEVI LGLQYGTайд MWSLGCILAE	
humdyrk4_dyr DFGSSCYEHQ K...VYTYIQ SRFYRSPEVI LGHPYDVAID MWSLGCITAE	
humdyrk2_np_ DFGSSCYEHQ R...VYTYIQ SRFYRAPEVI LGARYGMPID MWSLGCILAE	
humdyrk3_np_ DFGSSCFEYQ K...LYTYIQ SRFYRAPEII LGSRYSTPID IWSFRCILAE	
wormf49e11_q DFGSSCFDDQ R...IYTYIQ SRFYRAPEVI LGTKYGMPIД MWSLGCILAE	
kab7_schpo.k DFGSSCFYNE R...VYTYLQ SRFYRAPEII LGLEYGKEID IWSFGCILAE	
pom1_schpo.k DFGSSCFEGE C...VYTYIQ SRFYRSPEVI LGMGYGTPID VWSLGCIIAE	
humhipk4.kd. DFGSASIFSE VRYVKEPYIQ SRFYRAPEIL LGLPFCEKVD VWSLGCVMAE	
monkeyhipk4_ DFGSASIFSE VRYVKEPYIQ SRFYRAPEIL LGLPFCEKVD VWSLGCVMAE	
mushipk4.kd. DFGSASIFSE VRYVKEPYIQ SRFYRAPEIL LGLPFCEKVD VWSLGCVMAE	
rathipk4_xp_ DFGSASIFSE VRYVKEPYIQ SRFYRAPEIL LGLPFCEKVD VWSLGCVMAE	
250	
musdyrk1a_np MHTGEPLFSG ANEVQDMNKI VEVLGIPPAH ILDQAPKARK FFEKLPDGTW	
ratdyrk1a_np MHTGEPLFSG ANEVQDMNKI VEVLGIPPAH ILDQAPKARK FFEKLPDGTW	
humdyrk1a_np MHTGEPLFSG ANEVQDMNKI VEVLGIPPAH ILDQAPKARK FFEKLPDGTW	
humdyrk1b_np MHTGEPLFSG SNEVDQMNRI VEVLGIPPAА MLDQAPKARK YFERLPGGW	
musdyrk1b_np MHTGEPLFSG SNEVDQMSRI VEVLGIPPAП MLEQAPKARK YFERLPGGW	
dmmnb_aaf487 MHTGEPLFSG CNEVDQMNKI VEVLGMPPKY LLDQAHKTRK FFDKIVADGS	
wormt04c10_q MHTGEPLFAG SSEVDQMMKI VEVLGMPPKЕ MLDIGPKTHK YFDKTEDGIY	
dmsmi35a_q9v LYTGFPFLPG ENEVEQLACI MEVGLLPPKV LISVARRRRL FFDSRDAPRC	
humdyrk4_dyr LYTGFPFLPG ENEVEQLACI MEVGLLPPAG FIQTASRQQT FFDSKGFPKN	
humdyrk2_np_ LLTGYPPLPG EDEGDQLACM IELLMGMPSK LLDASKRAKN FVSSKGYPRY	
humdyrk3_np_ LLTGQPLFPG EDEGDQLACM MELLGMPPPK LLEQSKRAKY FINSKGIPRY	
wormf49e11_q LLTGYPPLPG EDENDQLALI IELLMGMPPK SLETAKRART FITSKGYPRY	
kab7_schpo.k LFTGVPLFPG GNETEQLGYI MEVLGPPPMA LIRNSTRSKA YFDSEGKPHP	
pom1_schpo.k MYTGFPLFPG ENEQEQLACI MEIFGPPDHS LIDKCSRKKV FFDSSGKPRP	
humhipk4.kd. LH LGWPLYPG NNEYDQVRYI CETQGLPKPH LLHAACKAHH FFKRNPHPDA	
monkeyhipk4_ LH LGWPLYPG NNEYDQVRYI CETQGLPKPH LLHAARKAHH FFKRNPHPDA	
mushipk4.kd. LH LGWPLYPG NNEYDQVRYI CETQGLPKPH LLHAARKAHH FFKRNPHPDA	
rathipk4_xp_ LH LGWPLYPG NNEYDQVRYI CETQGLPKPH LLHAARKAHH FFKRNPHPDA	

251	300	
musdyrk1a_np	SLKKT.....	K DGKREYKPPG TRKLHNILGV ETGGPGGRRA
ratdyrk1a_np	SLKKT.....	K DGKREYKPPG TRKLHNILGV ETGGPGGRRA
humdyrk1a_np	NLKKT.....	K DGKREYKPPG TRKLHNILGV ETGGPGGRRA
humdyrk1b_np	TLRRT.....	K ELRKDYQGPG TRLQEVLGV QTGGPGGRRA
musdyrk1b_np	TLRRT.....	K ELR.....
dmmnb_aaf487	YVLKK.....	N QNGRKYKPPG SRKLHDILGV ETGGPGGRRL
wormt04c10_q	YCKKTR.....	D GYRHTYKAPG ARKLHEILGV TSGGPGGRRL
dmsmi35a_q9v	ITNT..... KG RKRSPGSKS.
humdyrk4_dyr	ITNN..... RG KKRYPDSKD.
humdyrk2_np_	CTVTT..... LSDGSV VLNGGRSRRG KLRGPESRE
humdyrk3_np_	CSVTT..... QADGRV VLVGGRSRRG KKRGPPGSKD
wormf49e11_q	CTATS..... MPDGSV VLAGARSKRG KMRGPPASRS
kab7_schpo.k	ITDS..... HNRLLVPSTR
pom1_schpo.k	FVSS..... KGVSRRPFSK
humhipk4.kd.	ANPWQLKSSA	DYLAETKVRP LERRKYMLKS LDQIETVNGG SVASRLTFPD
monkeyhipk4_	ANPWQLKSSA	DYLAETKVRP LERRKYMLKS LDQIETVNGG SVASRLTFPD
mushipk4.kd.	TNPWQLKSSA	DYLAETKVRP LERRKYMLKS LDQIETVNGG GAVSRLSFPD
rathipk4_xp_	TNPWQLKSSA	DYLAETKVRP LERRKYMLKS LDQIETVNGG GAVNRLSFPD
301	340	
musdyrk1a_np	GESGHTVADY	LKFKDLILRM LDYDPKTRIQ PYYALQHSFF
ratdyrk1a_np	GESGHTVADY	LKFKDLILRM LDYDPKTRIQ PYYALQHSFF
humdyrk1a_np	GESGHTVADY	LKFKDLILRM LDYDPKTRIQ PYYALQHSFF
humdyrk1b_np	GEPGHSPADY	LRFQDLVLRM LEYEPAARIS PLGALQHGFF
musdyrk1b_np	KDLVLRM LEYEPAARIS PLGALQHGFF
dmmnb_aaf487	DEPGHSVSDY	LKFKDLILRM LDFDPKTRVT PYYALQHNFF
wormt04c10_q	GEPGHSVEDY	SKFKDLIKRM LQFDPKQRIS PYYVVVRHPFL
dmsmi35a_q9v	.LAHILHCQD	RYFIDFLQRC LEWDPAERMT PDEAAHHEFL
humdyrk4_dyr	.LTMVLUKYD	TSFLDFLRRC LVWEPSLRMT PDQALKHAWI
humdyrk2_np_	WGNALKGCDD	PLFLDFLKQC LEWDPAVRMT PGQALRHPWL
humdyrk3_np_	WGTALKGCDD	YLFIIEFLKRC LHWDPSARLT PAQALRHPWI
wormf49e11_q	WSTALKNMGD	ELFVDFLKRC LDWDPETRMT PAQALKHKWL
kab7_schpo.k	TFSQLLNTKQ	ASFIDFLSKC LKWDPKDRIT VDSALQHEFI
pom1_schpo.k	SLHQVLQCKD	VSFLSFISDC LKWDPPDERMT PQQAAQHDFL
humhipk4.kd.	REALAEHADL	KSMVELIKRM LTWESHERIS PSAALRHPFV
monkeyhipk4_	REALAEHADL	KSMVELIKRM LTWESHERIS PSAALRHPFV
mushipk4.kd.	REALAEHADL	KSMVELIKRM LTWESHERIS PSAALRHPFV
rathipk4_xp_	REALAEHADL	KSMVELIKRM LTWESHERIS PSAALRHPFV

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